

A study of Allogamy in wild *Phaseolus vulgaris*

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The common bean, *Phaseolus vulgaris*, has been considered as autogamous, that is, self-fertilizing. Several reports show, however, different percentages of allogamy (i.e., cross-fertilization). For genebank management it is of crucial importance to know an estimate of outcrossing rates in the multiplication fields, for maintaining the original genetic composition of accessions. This project studied the allogamy level among and within populations of wild *P. vulgaris* L. by using hypocotyl color as a genetic marker. A subsequent validation of the levels found was also carried out with biochemical marker, specifically peroxidase isozyme, found in young root tissue, attempting to find a correlation between the isozyme polymorphism with the morphological marker.

Six accessions of wild *P. vulgaris* were selected as male parents; the pigmentation (purple color) of their hypocotyls was used as genetic marker. Three accessions with unpigmented hypocotyls were chosen as female parents. The gene pools (Mesoamerica, northern Andes, and southern Andes) to which they belonged were also considered.

The populations were planted in a CIAT location (Corregimiento El Moral-Cerrito, Colombia, at 3° 44' N, 76° 5' W; 2,000 m.a.s.l.; 13.6°C average annual temperature; 1,181 mm average annual rainfall) under open-pollination conditions. A split-plot experimental design was used in which the main plot carried the male parent, surrounded by three females. Four replicates were used, corresponding to four terraces with an 18% slope. Each terrace was isolated by a natural barrier of *P. lunatus*. The seed produced by the females, which received pollen from males with pigmented hypocotyls, was analyzed for the level of allogamy, or inter-crossability, among accessions.

Among the F_1 from the females progeny a few individuals with pigmented hypocotyls appeared, suggesting that outcrossing occurred. In fact, for the 30,388 F_1 progeny seeds planted in the greenhouse, the average percentage of outcrossing was 1.5%, and although, a wide coefficient of variation was present, the northern Andes genepool always appeared with the highest drates of crossability with Mesoamerica and southern Andes. Duncan's Multiple Range Test indicated that the highest crossability rate, 8.62%, was found between populations from Mesoamerica and northern Andes. For populations from northern Andes and southern Andes, the highest crossability rate was 1.28%, whereas populations from Mesoamerica and southern Andes the highest crossability rate was 0.71%; within gene pools, the highest rate, 2.18%, was found within northern Andes (Table 1). The contrast test showed significant differences of allogamy between Mesoamerica and northern Andes populations. The analysis also suggested an effect of replication

(terraces), perhaps because of factors such as wind, insects, or microclimates. The lowest terrace had the highest crossability rate (3.3%).

To study intra-crossability among accessions, a northern Andes population was selected. The original population had both pigmented and unpigmented hypocotyls in a 2:3 ratio. Unpigmented females were surrounded by pigmented males, and the field was protected by a natural barrier of *P. lunatus*. The average outcrossing rate was 8.73%.

An electrophoretic analysis of young root tissue, using peroxidase isozyme, suggested the possible presence of two loci controlling hypocotyl color. Locus PRX-1 from male parents gave the pigmented hypocotyl, whereas locus PRX-2 from female parents gave the unpigmented hypocotyl. Analysis of the progeny showed a 12.9% of hybrids between loci PRX-1 and PRX-2. Some of the progeny, however, with either pigmented or unpigmented hypocotyls had no bands for PRX-1 or PRX-2.

Table 1. Rate of allogamy tested in F₁, from 18 parental combinations.

Female parental/ (Country of origin) #	Male parental / country of origin						Female General Mean. (%)
	G 12949 A (MEXICO) ♂ 5	G 19906 (GUATEMALA) ♂ 4	G 23435 (GUATEMALA) ♂ 1	G 21117 (COLOMBIA) ♂ 6	G 21244 (PERU) ♂ 2	G 21194 (ARGENTINA) ♂ 3	
C G 23465 (MEXICO)	0.07	1.15	0.28	6.07	0.42	0.70	1.41
A G 22303 (COLOMBIA)	0.43	8.62	1.14	2.18	1.28	0.93	2.43
B G 23457 (PERU)	0.28	0.63	0.63	0.42	0.42	0.57	0.50
Male General Mean (%)	0.30	3.43	0.66	2.79	0.76	0.75	1.50